



seer

J.P. MORGAN HEALTHCARE CONFERENCE

January 2023

Safe harbor disclosures

Certain statements in this presentation and the accompanying oral commentary are forward-looking statements within the meaning of the federal securities laws. These statements relate to future events or Seer, Inc. (the “Company”)’s future results and involve known and unknown risks, uncertainties and other factors that may cause the actual results, levels of activity, performance or achievements of the Company or its industry to be materially different from those expressed or implied by any forward-looking statements. In some cases, forward-looking statements can be identified by terminology such as “may,” “will,” “could,” “would,” “should,” “to,” “target,” “expect,” “plan,” “anticipate,” “intend,” “believe,” “estimate,” “predict,” “potential” or other comparable terminology.

All statements other than statements of historical fact could be deemed forward-looking. These forward-looking statements are subject to a number of risks, uncertainties and assumptions, including, among other things: any expectations regarding the Company's projections of market opportunities; statements regarding the Company's business strategy, operations, results of operations, financial needs, and financial condition; statements regarding the Company's long-term expectations; statements that may suggest trends for the Company's business or industry, including expectations that may affect the unmet need and the size of the proteomics market and adjacent markets; statements about the Company's broad commercial release, consortium arrangement, centers of excellence, enablement of future clinical validation, statements about the Company's ability to successfully commercialize the Proteograph™ Product Suite, demand for the Proteograph Product Suite; the launch of any new or additional products, any expectations or statements regarding domestic or global markets, including but not limited to Europe and Asia; statements regarding customer adoption of new technologies domestically and globally; the Company's ability to expand life sciences markets through the use of its technology; the discovery of new protein variants and novel biomarkers leading to therapeutic breakthroughs, the scope of protection the Company is able to successfully establish and maintain for intellectual property rights, including its Proteograph Product Suite, and the number of patents and claims issued, pending or granted; projections, assumptions, and estimates of the Company's future performance and the future performance of the markets in which it operates; the Company's expectations regarding its gross margins, and operating income and expenses; any statements of the plans, strategies, and objectives of management for future operations; any statements of expectation or belief regarding future events, opportunities to drive future growth, and potential markets or market size, or technology developments.

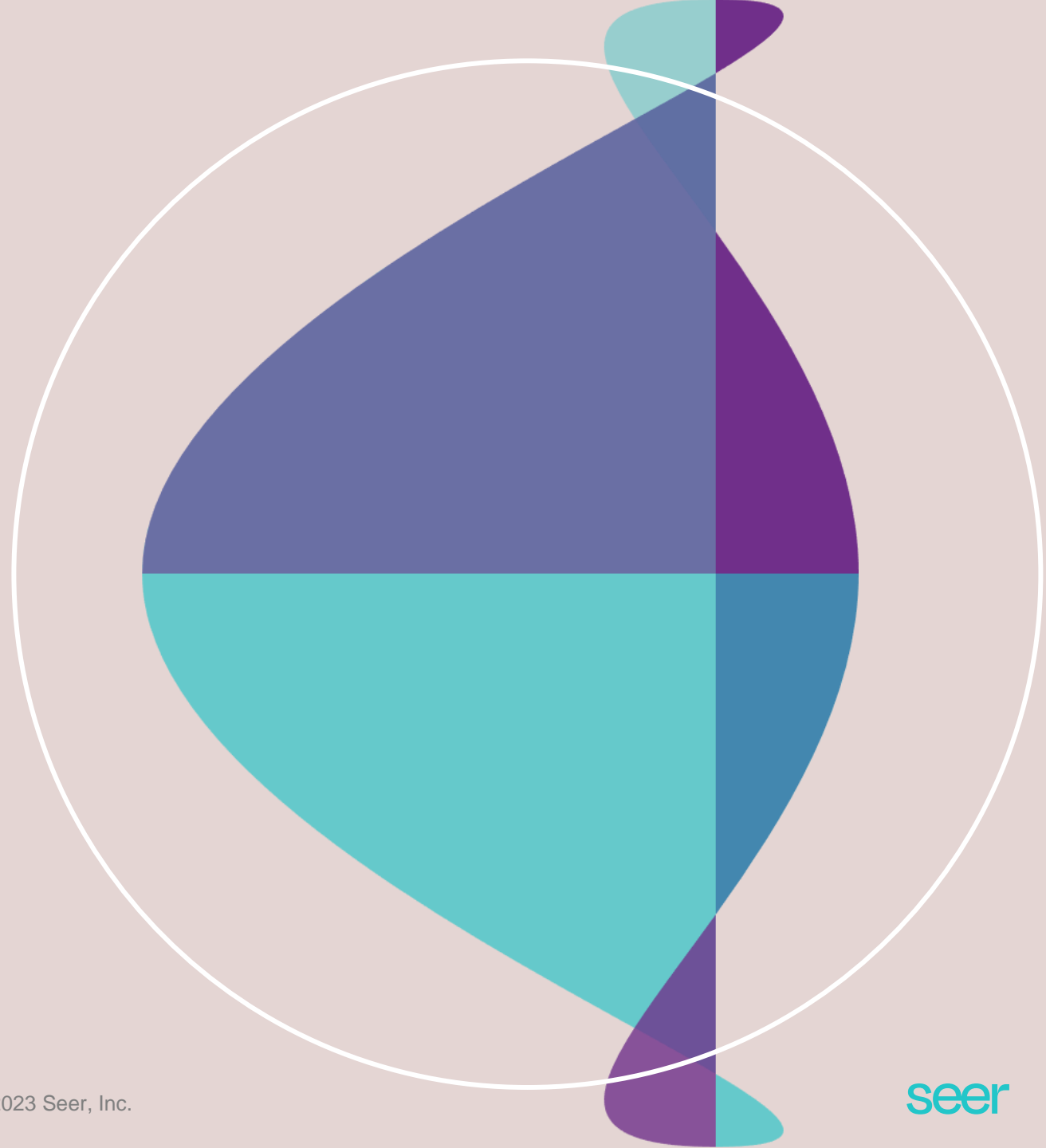
While the Company believes these expectations, assumptions, estimates and projections are reasonable, such forward-looking statements are only predictions and involve known and unknown risks and uncertainties, many of which are beyond the Company's control. These and other important factors may cause actual results, performance, or achievements to differ materially from those expressed or implied by these forward-looking statements. The forward-looking statements in this presentation are made only as of the date hereof. For a further description of the risks and uncertainties that could cause actual results to differ from those expressed in these forward-looking statements, as well as risks relating to the business of the Company in general, are described more fully in the Company's filings with the Securities and Exchange Commission (“SEC”) and other documents that the Company subsequently files with the SEC from time to time. The Company specifically disclaims any intention to update any forward-looking statements included in this presentation. If one or more of these statements is updated or corrected, investors and others should not conclude that additional updates or corrections will be made.

In light of the foregoing, investors are urged not to rely on any forward-looking statement in reaching any conclusion or making any investment decision about any securities of the Company.

We imagine and
pioneer new ways to

decode the secrets of the proteome

to improve human health





Changing the trajectory of deep, unbiased proteomics



Enabling customers to access deep, unbiased, rapid proteomics at scale



Broadly accessible and durably differentiated technology

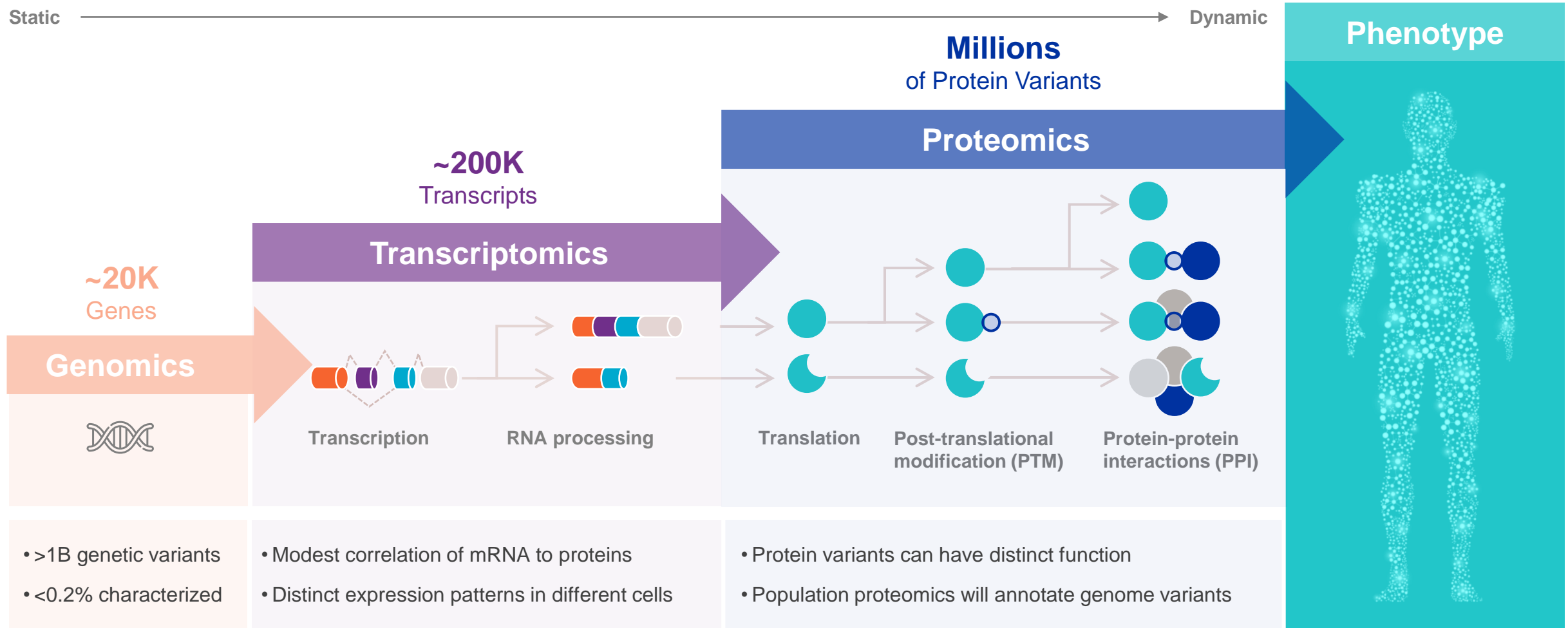


Large potential market opportunity across proteomics, genomics and new end markets



Management team uniquely positioned to capitalize on proteomics

Full characterization of the proteome is essential



Source: Isabell Bludau et al. Proteomic and interactomic insights into the molecular basis of cell functional diversity. Nature Reviews Molecular Cell Biology (2020).

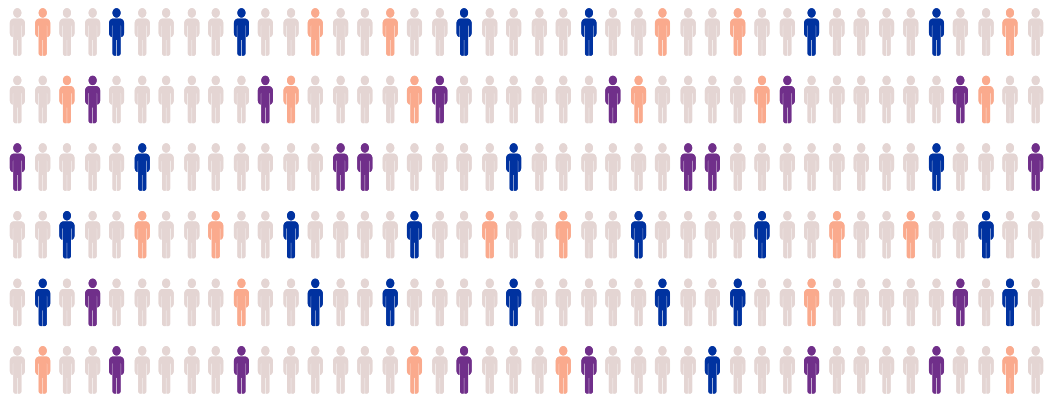
Functional implication of protein variants across the population is massive

Single individual (~20,000 genes)



Protein variants per participant	9,506
Potential deleterious variants	2,945
Protein loss of function	214
Alternative splice forms	95% of genes

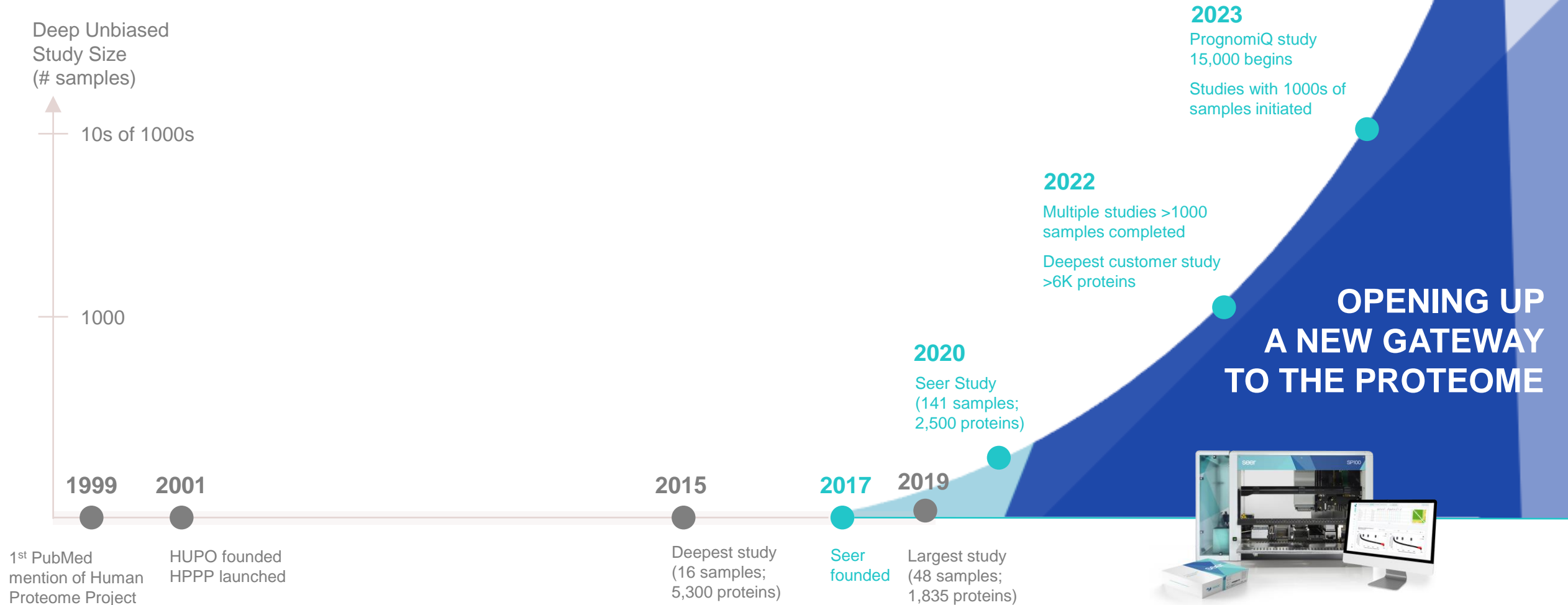
Population (~455,000 individuals)



All protein genetic variants	8,868,971
Potential deleterious variants	6,345,457
Protein loss of function	915,289
Change protein structure/binding	> 3 million

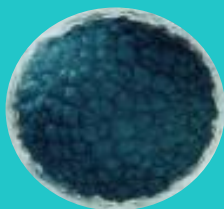
Source: Backman, J.D. *et al.* Exome sequencing and analysis of 454,787 UK Biobank participants. *Nature* **599**, 628–634 (2021)

Changing the trajectory of deep unbiased proteomics



Seer enables unbiased, deep and rapid proteomic analysis at scale

Taking advantage of the way proteins interact



Lab on a nanoparticle



Unbiased

Deep

Rapid

Large-scale

seer

A new gateway
to the proteome



Delivering unique benefits

- High accuracy and reproducibility
- Quantitative measurement
- Broad dynamic range
- 1% False Discovery Rate (FDR)
- Wide range of sample types
- Species agnostic
- Novel biological insight

Seer is positioned to lead the proteomics revolution

Establishing
Seer as the
premier provider
in proteomics

Enabling unique
applications and
insights

Empowering
at scale, first-of-
their-kind
studies


Making deep,
unbiased
proteomics
accessible to
more labs



Opening a new frontier in biology

Expanding proteomics and genomics markets via unbiased, deep, and rapid proteomics at scale


Genomics
~\$21B


Proteomics
~\$32B

Unmet need for deep, unbiased proteomics at scale

Academic

Translational

Commercial

Pharma

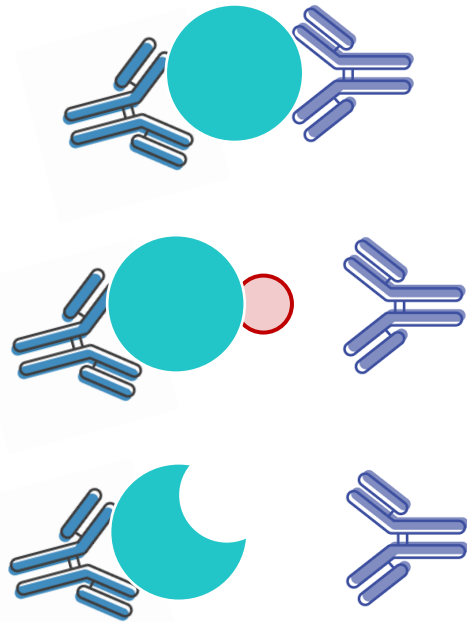
Applied

Source: UniProt, PNAS, PLOS

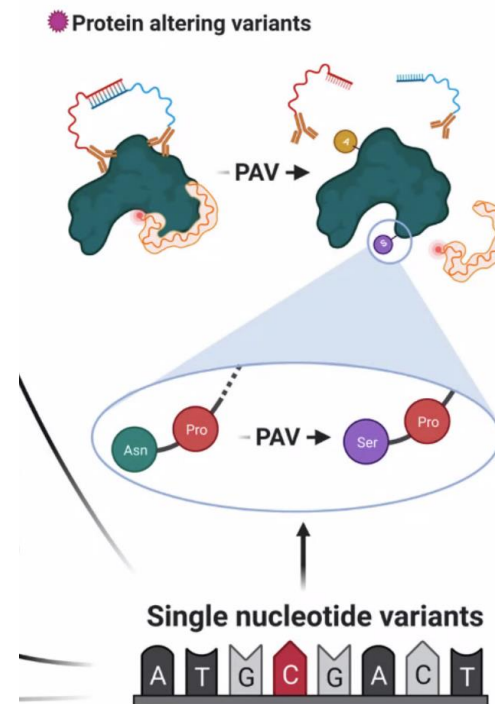
Protein variants are a challenge for affinity-based approaches

Affinity-Based Approaches

Low Correlation for the Same Protein (0.38)



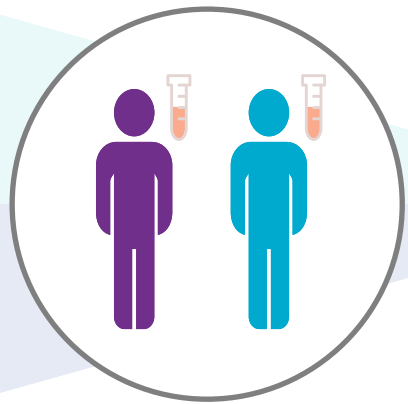
Three Protein Variants
Epitope Location Unknown



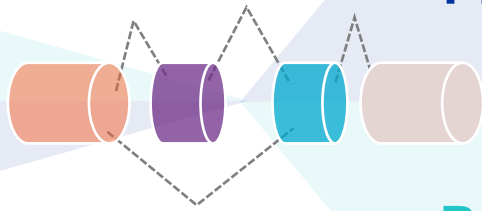
"Protein-phenotype colocalization...goes beyond missing target specificity and can be explained by alternative proteoforms induced by genetic variants altering the amino acid sequence of the protein and the effects of alternative splicing"

Pietzner, et al
Nature Communications,
Nov 2021

Peptide level resolution may reveal protein splice variants

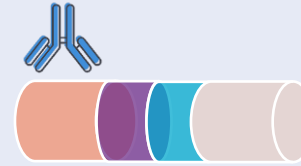


Multiple protein splice variants can arise from the same gene locus

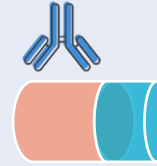


Protein Level

Peptide Level



Splice variant 1



Splice variant 2

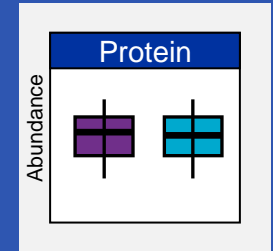


Splice variant 1

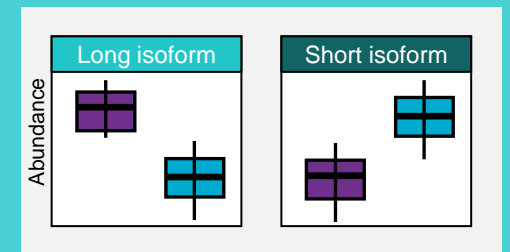


Splice variant 2

Differences missed



Meaningful differences detected



Peptide level analysis reveals NSCLC-associated protein splice variants

BMP1

Lacks collagen secretion domain; collagen protective in cancer^{1,2}

COL18A1

Endostatin, shown to treat NSCLC together with radiation^{2,3}

VWF

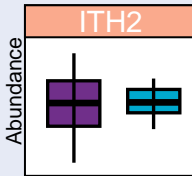
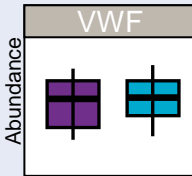
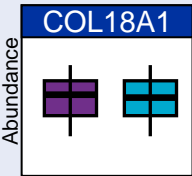
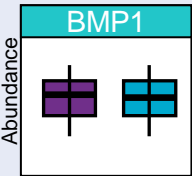
Elevated in NSCLC patients with poor prognosis⁴

ITH2

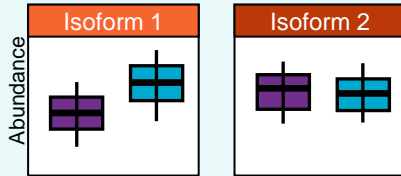
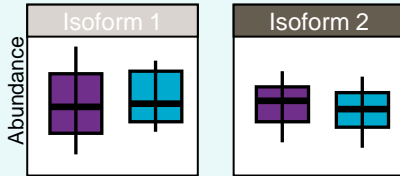
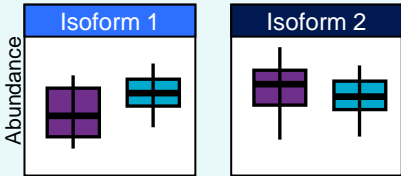
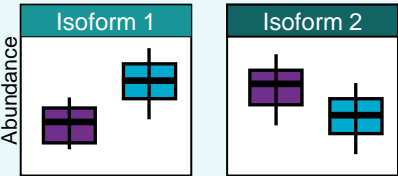
Downregulation may drive malignancy progression⁵



Protein Level

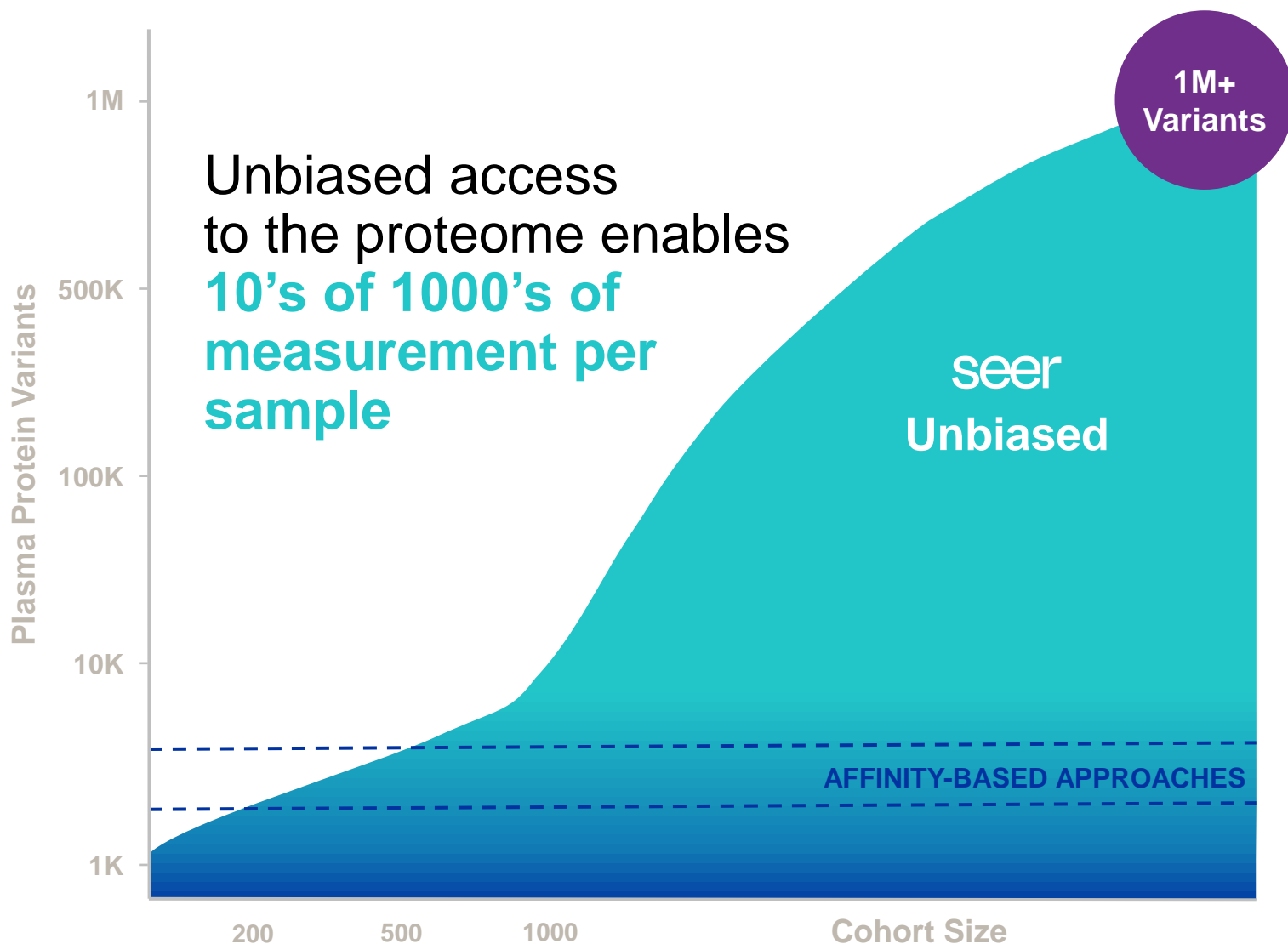


Peptide Level

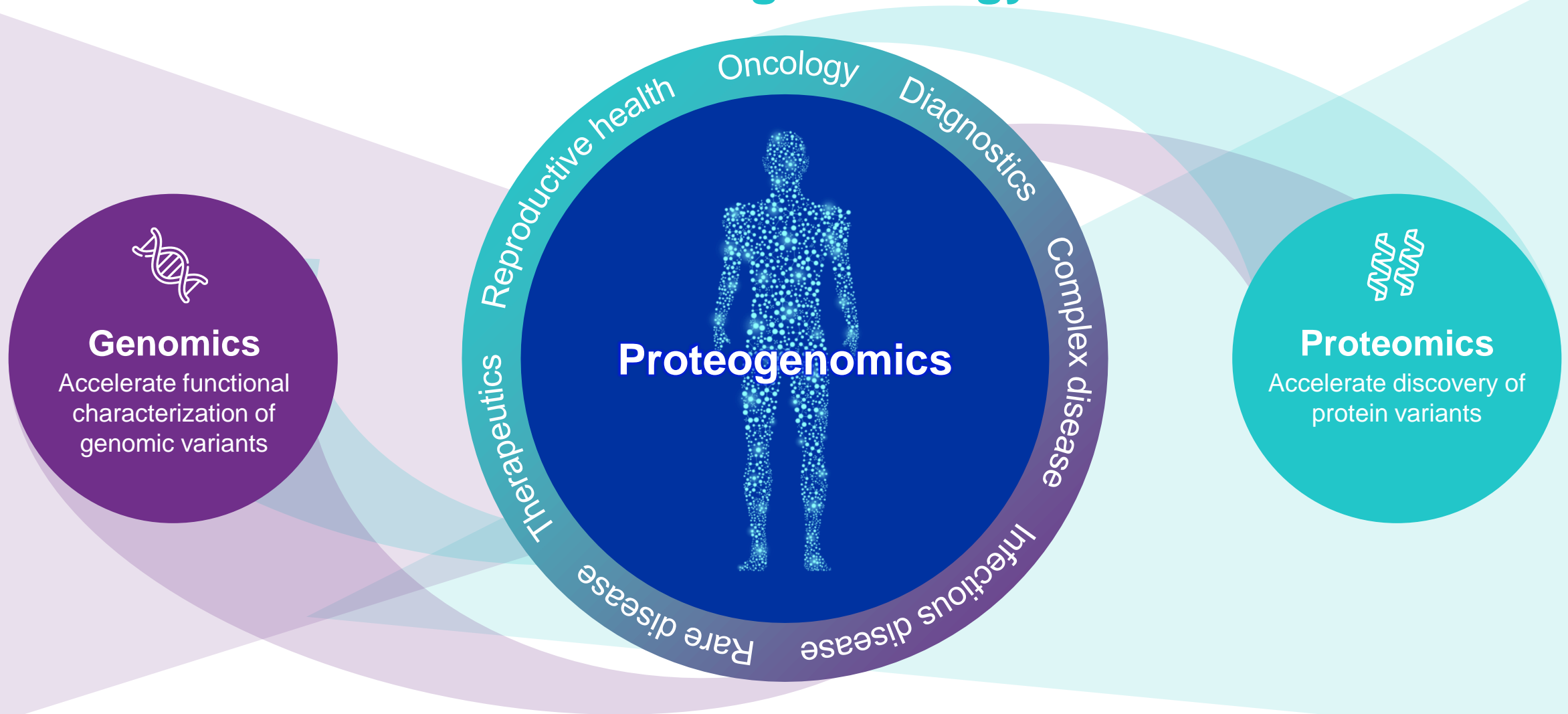


1. Chen Y et al., Cancer Cell (2021)
2. Donovan M (Seer) et al., in review (2022)
3. Zhang et al. Radiation Oncology (2020)
4. Guo et al. J Clin Lab Anal. (2018)
5. Hamm et al. BMC Cancer (2008)

Discovery of novel protein variants requires an unbiased approach



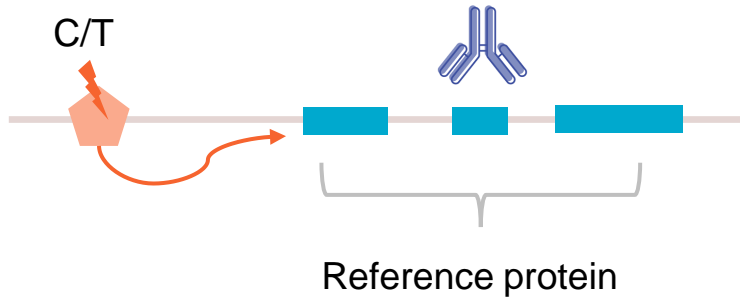
Deep, unbiased proteomics will enable proteogenomics and accelerate our understanding of biology



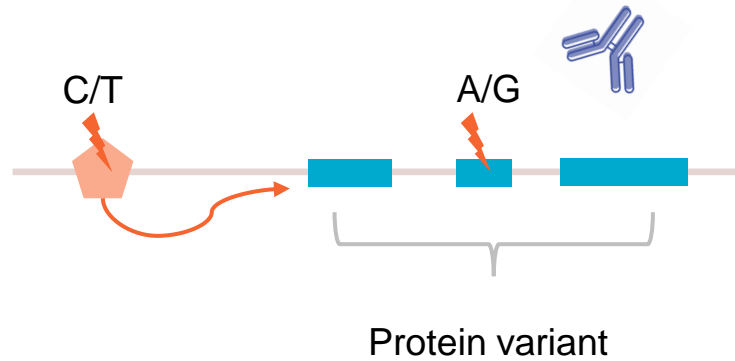
Accurate proteogenomics requires peptide-level resolution

Affinity-Based Approaches

True *cis*-pQTL

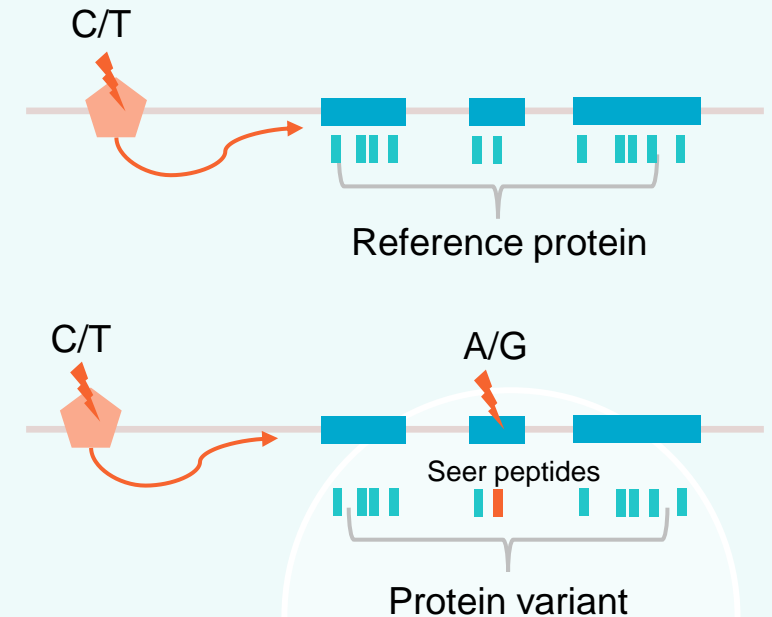


False *cis*-pQTL



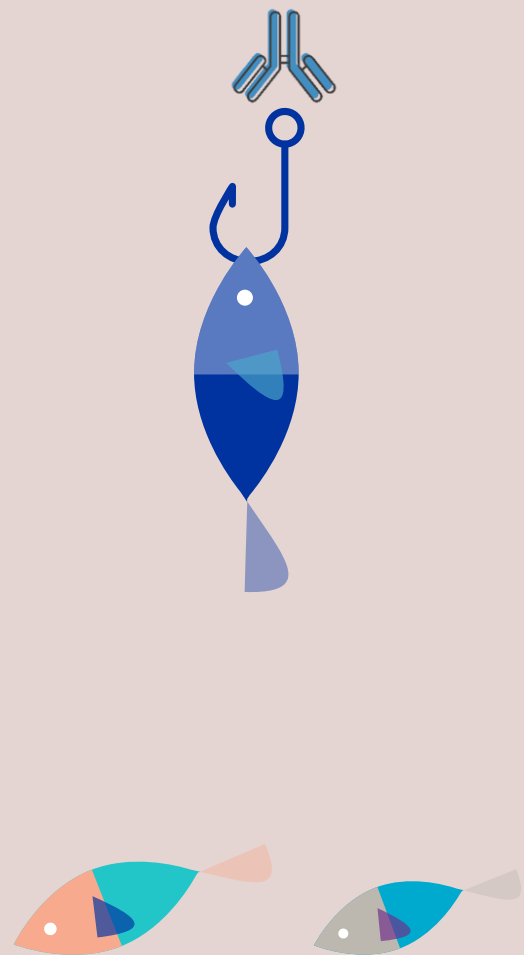
seer

Accurate biological insight True pQTLs

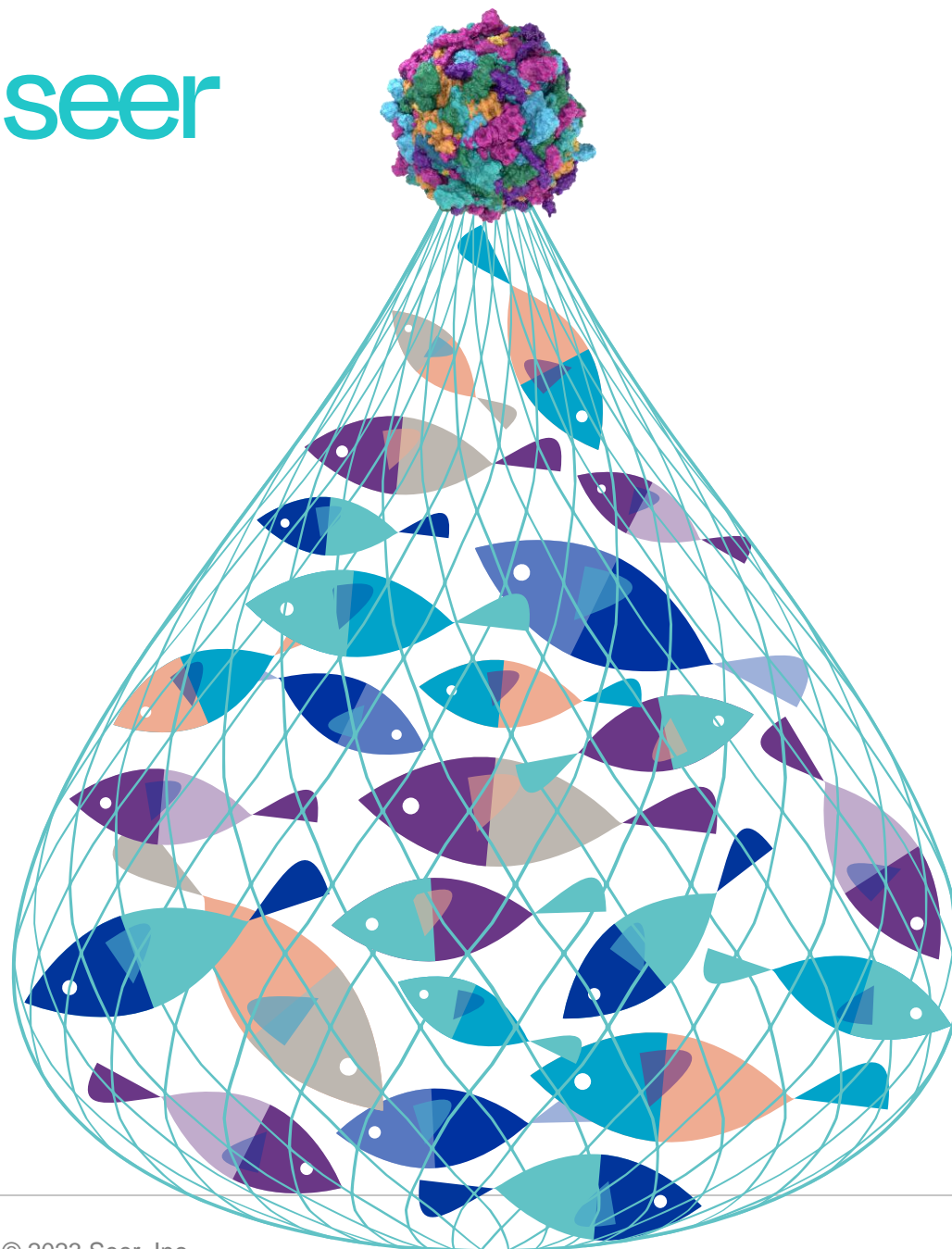


Protein variants cause false associations in affinity-based approaches

Affinity-based



seer



Strong execution in 2022



Highly differentiated solution

- ✓ Proteograph Product Suite performing exceptionally well in customers hands
- ✓ Validated utility across species, sample types, and low input volumes
- ✓ Launched Proteograph Analysis Suite 2.0
- ✓ Placed next product in the hands of early access customers
- ✓ 35 patents issued, >90 patents pending, representing ~7,500 claims



Growing revenue and strong balance sheet

- ~\$11 million revenue in first nine months of 2022¹
- ~\$441 million cash & cash equivalents and no debt¹



Demonstrated global commercial traction

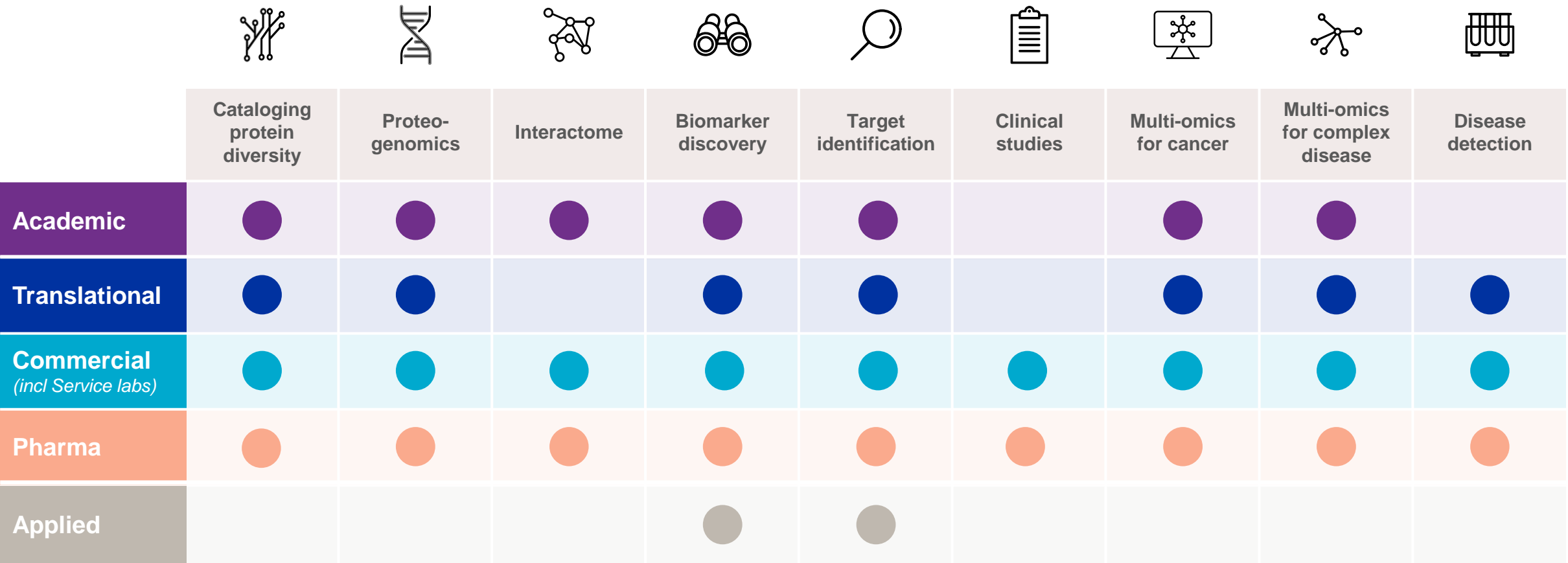
- ✓ Initiated Broad Commercial Release
- ✓ More than doubled revenue and installed base YoY
- ✓ Commercial presence in US and Europe
- ✓ Commercial partners in China and Korea



Continuing to attract and retain world class talent


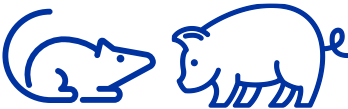



- 165+ FTEs at year end 2022

Gaining momentum across customers and applications

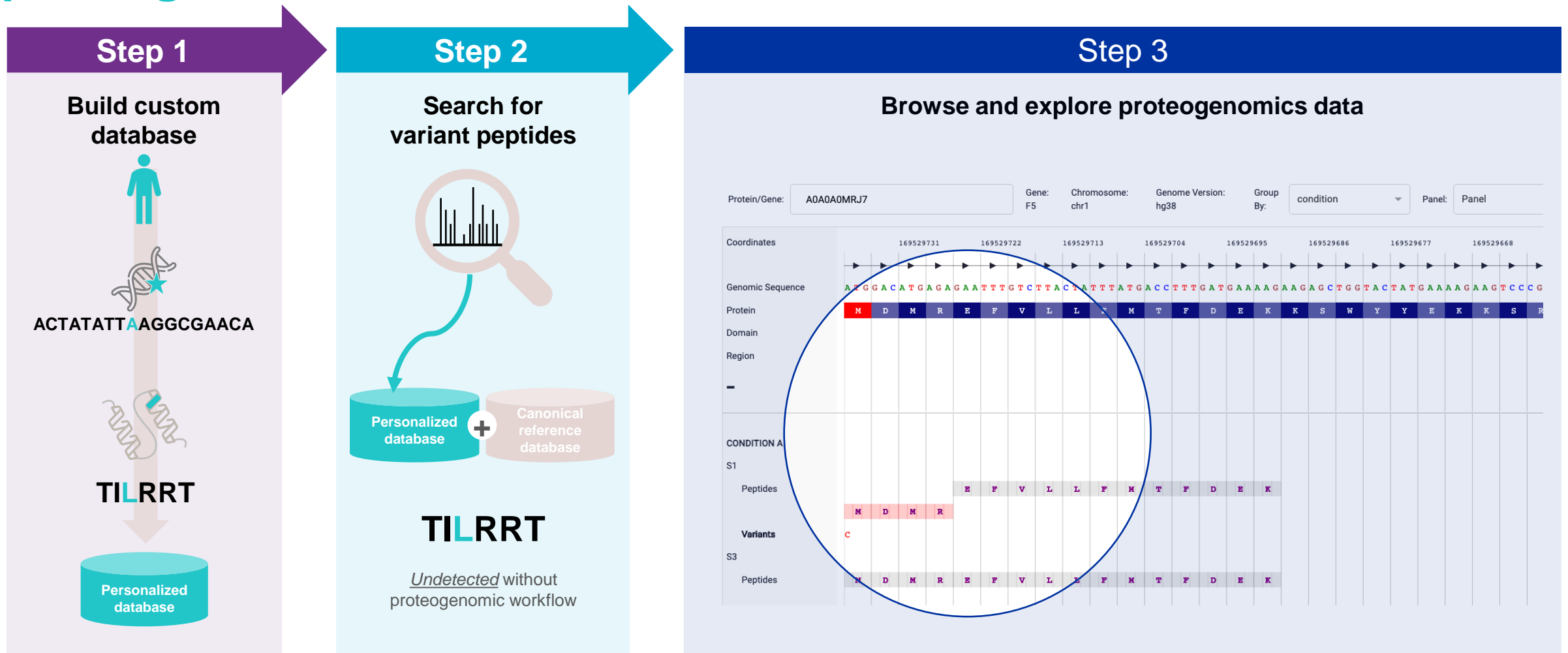


● Customer projects using the Proteograph in progress or completed

Enabling unbiased, deep proteomics across different sample types

					
Sample type	Human plasma	Model organisms	Urine	CSF	Conditioned media
Improvement Seer vs. neat biofluids	4x	4x	1.5x	1.5x	8.6x
10s of 1000s of data points 1000s of proteins per sample					

PAS 2.0: Paving the way for high-resolution, proteogenomics at-scale



The Proteogenomics workflow enables the discovery of novel, sample-specific variant peptides

Seer-designed data tools to power at-scale studies

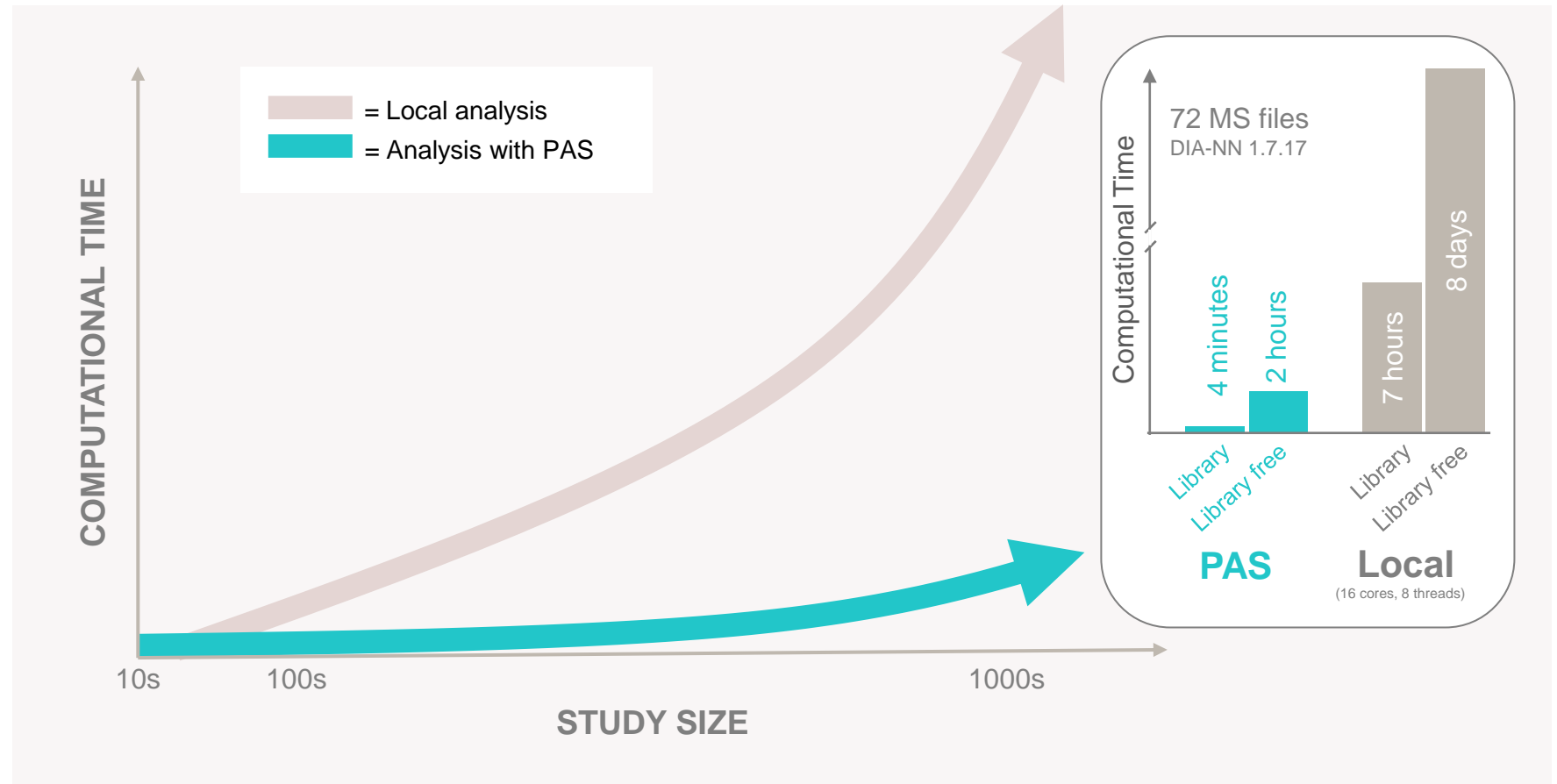
Seamless journey from raw data to insight

Cloud **scalable architecture**

Pre-configured **data pipelines**

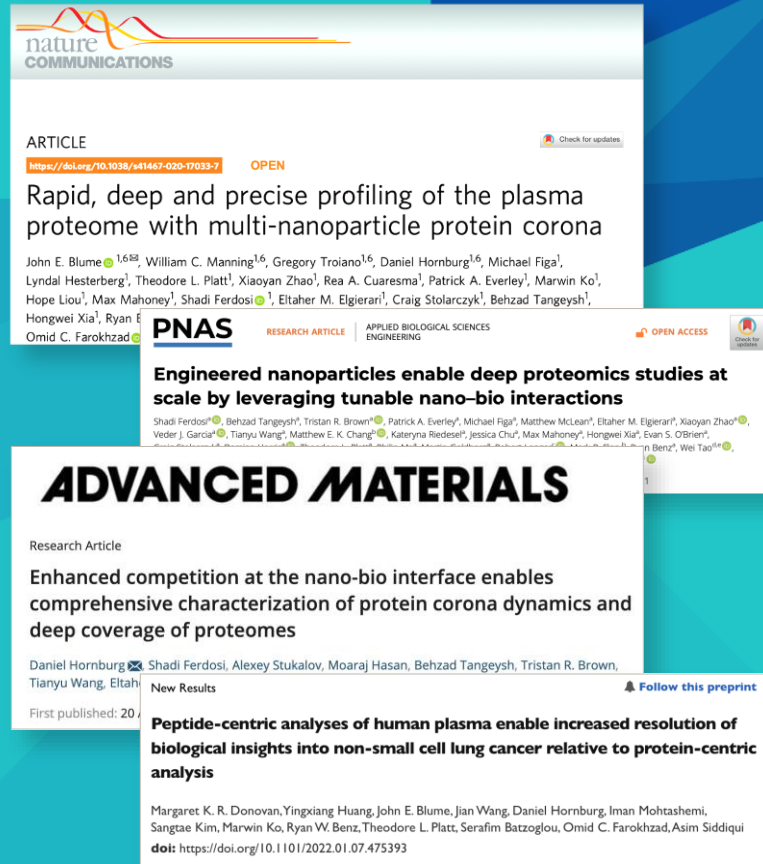
Batch effects correction

Automatic data upload



Paving the way to get to insights faster

Growing external validation of Seer technology



119

Poster presentations
at conferences

19

Poster presentations
by customers

20

Oral presentations
at events



Science & Technology
Award from HUPO



TheScientist
TOP10
INNOVATIONS

#4 on Top 10 Innovations
of 2022 by The Scientist

Why researchers are using the Proteograph Product Suite



Jon Brudvig, Ph.D.

Assistant Professor, Pediatrics
Pediatrics and Rare Diseases Group
Sanford Research

"Working with Seer has transformed our multi-omics biomarker discovery initiatives. Seer's Proteograph is allowing us to generate unbiased, quantitative data for over 3000 pig plasma proteins, enabling us to find new biomarker signatures of slow-progressing diseases like CLN3 Batten Diseases in animal models."

Publication pending



Joshua Coon, Ph.D.

Professor of Chemistry and
Biomolecular Chemistry
at University of Wisconsin–Madison

"We are very excited to leverage Seer technology to enable deep and fast plasma proteome analysis. The ability to profile thousands of proteins in a discovery manner within an hour from plasma is unprecedented. This capability has redefined how we think about leveraging mass spectrometry on myriad clinical and translational projects."

*Data presented at HUPO World
2022 Congress*



Neil Kelleher, Ph.D.

Professor of Chemistry,
Molecular Biosciences,
and Medicine at
Northwestern University

"As we advance on the equivalent of the Human Genome Project for protein-level biology, industry partners like Seer are playing a critical role and accelerating the arrival of next-generation proteomics technologies."

*Seer joins consortium - Human
Proteome project*



Jennifer Van Eyk, Ph.D.

Professor of Medicine and
Biomedical Engineering, Director,
Precision Biomarker Laboratories
Cedar-Sinai Cancer Institute

Collaboration leveraging Proteograph for quantification of clinically-related markers that are unavailable as immunoassays in combination with a high-throughput LCMS method would allow quantification of personalized clinically-related markers.

*Data presented at NIDDK, TAMADOR
2022 meeting
Publication pending*



Karsten Suhre, Ph.D.

Professor of Physiology and
Biophysics and Director of the
Bioinformatics Core at Weill
Cornell Medicine - Qatar

"Having unbiased access to the proteome with peptide-level insights is necessary to truly understand the proteome, its variants and its connection to human health and disease. Myself and my colleagues at WCM-Q were very satisfied that the Seer Proteograph technology was able to provide this."

Publication pending

Operationalizing the Proteogenomics Consortium

Discovery Life Sciences Launches World-Class Proteomic Services Division Supported By Leading Technology Partners

Creates a single source for large-scale population studies, biobank characterization, and multi-omic biomarker analysis to support drug and diagnostic development

December 14, 2022



Proteograph Product Suite

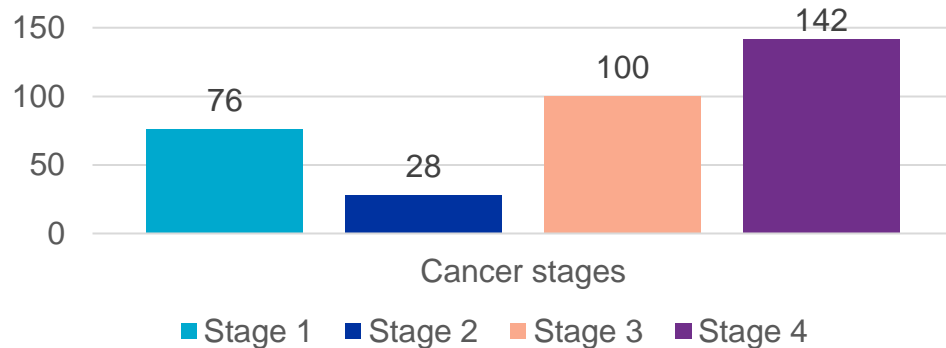
ZenoTOF 7600

Bringing proteomics to genomics customers

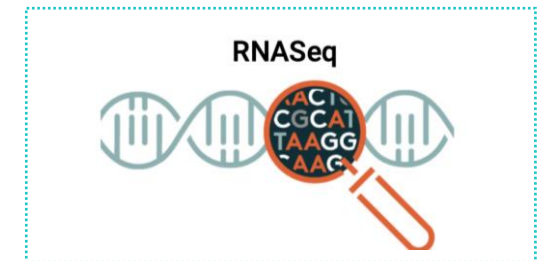
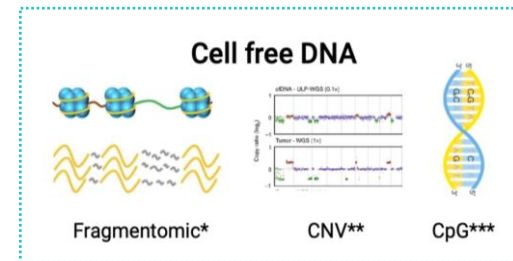
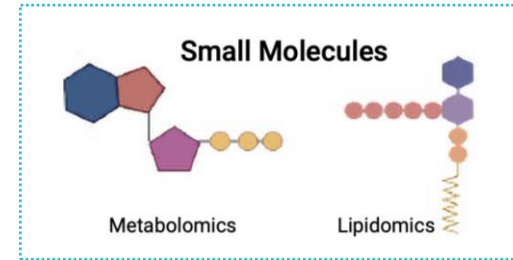


Proteograph Product Suite powers largest deep multi-omics study to date of 1,031 samples

- Enabled by the Proteograph Product Suite
- Age and gender balanced
- 371 cancer vs 670 non-cancer
- Multi-omics on all plasma samples
- Initiated enrollment of 15,000 subject study



Integrative Multi-omics

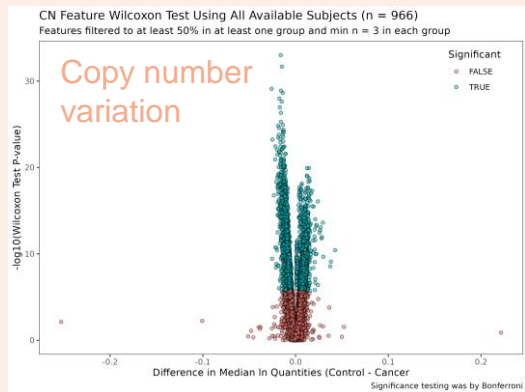
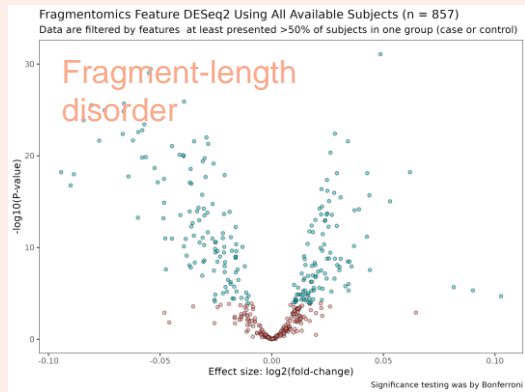


“I’m excited about these early results in lung cancer, where there is such a high unmet need for earlier detection and treatment, and with PrognomiQ’s potential to transform the performance of liquid biopsies using a multi-omics approach for lung and other lethal cancers,”

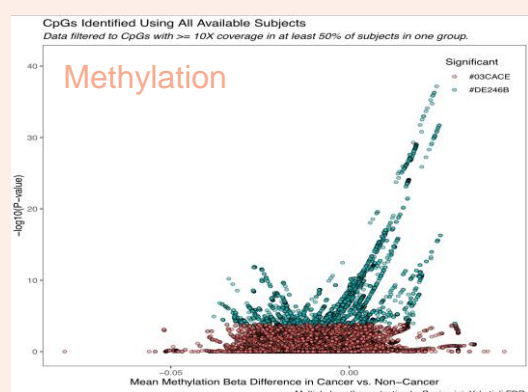
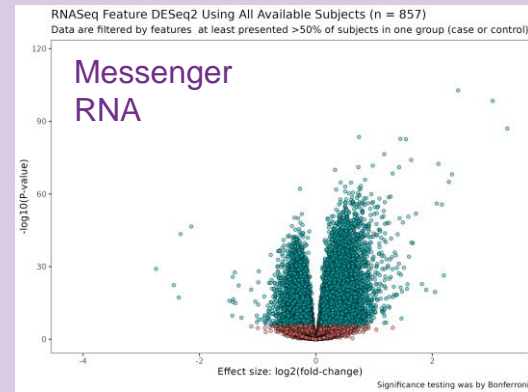
Luis A. Diaz, Head of the Division of Solid Tumor Oncology, Memorial Sloan Kettering

Strong performance for early-stage detection of non-small cell lung cancer

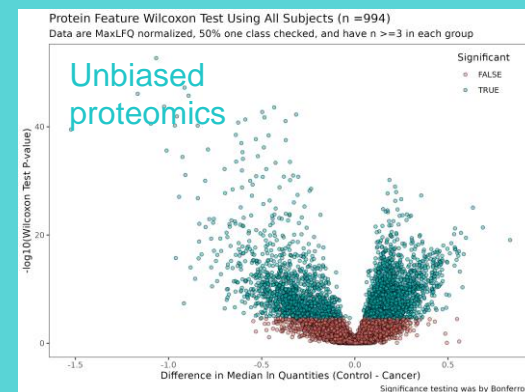
Genomics/Epigenomics



Transcriptomics

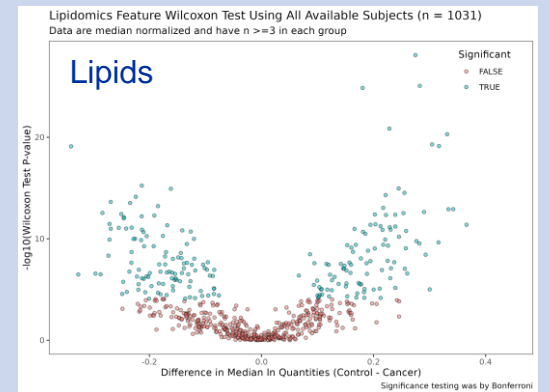
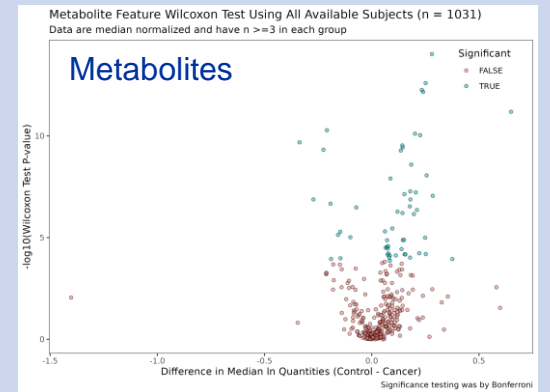


Proteomics



seer

Metabolites/Lipids



● Adj. $P \leq 0.05$ (statistically significant) ● Adj. $P > 0.05$

Univariate tests on difference in medians between non-cancer and cancer cohorts. Bonferroni is used to correct for multiple hypotheses testing except for methylation CpG analyses, where Benjamini-Yekutieli is used instead.

Looking ahead to 2023



Enable breakthrough science

- Accelerate population-scale studies
- Empower customers to drive biological insight from decoding the proteome
- Expand installed base
- Continue to expand access through Center of Excellence partners



Catalyze new applications and markets

- Broadly enable proteogenomics
- Obtain ISO 13485 certification to enable future clinical validation of Proteograph
- Leverage unique capabilities in model organisms and animal science



Demonstrate the power of the Proteograph Product Suite

- Execute against product roadmap with launch of new assay product
- Enhance PAS feature set for large-scale proteogenomics studies
- Increase presentations and peer-reviewed publications from customers



Expand our industry-leading team

- Continue to recruit top talent
- Expand global capabilities to support growing installed base



seer

Q&A